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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/508,821	05/26/2000	GUY A. ROULEAU	2055MC/48747	1968

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EXAMINER

GOLDBERG, JEANINE ANNE

ART UNIT

PAPER NUMBER

1655

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DATE MAILED: 01/28/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

## Notice to Comply

Application No.

09/508,821

Examiner

Jeanine Enewold Goldberg

Applicant(s)

ROULEAU ET AL.

Art Unit

1655

### NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

#### Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.
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EXAMINER

Jeanine Enewold Goldberg

ART UNIT	PAPER
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1655

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Commissioner of Patents and Trademarks

The communications filed November 9, 2001 and November 27, 2001 is not fully responsive to the Office communication mailed December 26, 2000 and May 9, 2001.

A) The specification has not identified all sequences which have more than 10 nucleotides with a SEQ ID NO. For example, on page 9, CAGCAA(CAG)10CAA is presented but is neither identified by SEQ ID NO: nor in the sequence listing. Similarly, the Claim 1 is directed to a string of nucleotides which are not identified by SEQ ID NO:, nor are present in the sequence listing.

B) As provided in MPEP 2421.02, Table 1, the one-letter code for A or G is R. Therefore, the identification of an A or G with a U in Claim 1 is inappropriate. Appropriate correction is required.

C) Further, it is noted that Applicants have amended the Sequence listing to include new SEQ ID NO: 6-10. Applicants submit that the substitute sequence listing is provided to show the hGT1 amino acid sequence. As provided on page 5 of the response, "The pertinent portion of SEQ ID NO: 5 has been translated. Support for the translation of SEQ ID NO: 5 can be found in the specification at page 8, lines 30-32, describing the 5535 bp open reading frame. Support can also be found at page 8, lines 35 to page 9, line 2, describing the 490 bp intro preceding the ORF".

The specification teaches the GT1 sequence includes a 5535 bp open-reading frame (ORF) of 5535 bps without interruption (page 8, lines 30-32). The specification teaches that the ORF is preceded by a 490 bp intron (including a consensus splice acceptor) and 19 bps of 5'UTR. The entire ORF may be coded for by a single exon (we are still missing the sequences coding for the last 12 amino acids (36 bp)) (page 9, lines 2-4).

While SEQ ID NO: 5 has been supported by the original disclosure (Figure 4A-4E), it appears as though the introduction of the protein (SEQ ID NO: 6) sequence is not supported by the original disclosure. Based upon the text of the specification, it appears as though there are 490 bp plus 19 bps prior to the ORF, such that there are 509 bps prior to the translation start site. The amendment which has added the protein sequence appears to begin at nucleotide position 490. Therefore, there is neither a 490 bp intron preceding the ORF nor the 490 bp intron and 19 bps of the 5'UTR. Thus, insertion of a start site at position 490 does not appear to be supported by the original disclosure.

Furthermore, as provided in the brief description of the drawings, Figure 4 illustrates the nucleotide sequence of hGT1, wherein the upstream intron is in lowercase; human gene sequence (exon) is in upper case; and the transcription start site ATG in bold. The examiner does not see a bolded start site.

Moreover, SEQ ID NO: 5 contains numerous three letter 'tga' sites (stop codons) in the "coding sequence". This is indicative that this is not a coding region. SEQ ID NO: 6-10 are fragments from the start to stop sites, which are not supported by the original disclosure nor the original figures.


The examiner requests further explanation of the Sequences and their support in the originally filed disclosure.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of **ONE (1) MONTH** from the mailing date of this communication within which to correct the

deficiency so as to comply with the sequential rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Any inquiry concerning this communication should be directed to Examiner **Jeanine Enewold Goldberg**, Art Unit 1655, whose telephone number is **(703) 306-5817**.

Any inquiry of a general nature or relating to the status of this application should be directed to the Technology Center receptionist whose telephone number is (703) 308-0196.

  
**BRADLEY L. SISSON**  
**PRIMARY EXAMINER**  
**GROUP 1800/1650**